

EXHIBIT 2

# IEDB Analysis Resource

Antibody Epitope Prediction

Example Sequences

Tutorial

External Links

Disclaimer

Reference

Contact

## Kolaskar & Tongaonkar Antigenicity

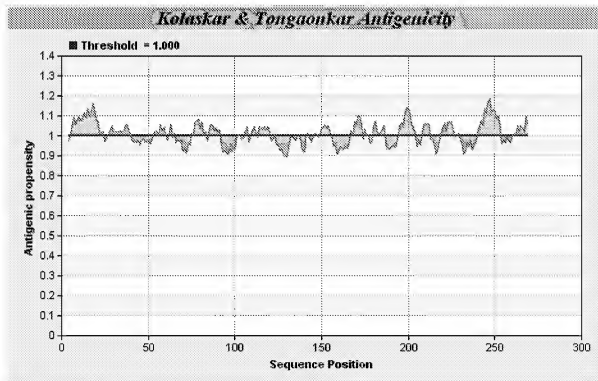
### Sequence:

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAASAAA  QCDTSSIGST  MQQASYAMGV
61  DIGRSLKQMK  EQGAELDLKV  FIDAMQAVYD  GKEIKMTEEQ  AQEVMMKFLQ  EQQAKAVEKH
121 KADAKANKER  GEAPLKENAA  KDGVATTASG  LQYKITKQGE  GKQPTRDDIV  TVEYEGRLID
181 GTVFDSSKAN  GGPATFFLSQ  VIPGWTEGVR  LLKEGGEATF  YIFSNLAYRE  QGAGEKIGPN
241 ATLVFDVKLV  KIGAPENAPA  KQPDQVDIKK  VN

```

Center position: 4 Window size: 7



Average: 1.010 Minimum: 0.897 Maximum: 1.184 Threshold: 1.000

[Click here to view plotted values in table format](#)

### Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	5	24	FKISALTLSAALALSACGKK	20

2	27	39	APASASEPAAASA	13
3	53	60	QASYAMGV	8
4	77	83	DLKVFTD	7
5	85	91	MQAVYDG	7
6	114	120	AKAVEKH	7
7	149	155	SGLQYKI	7
8	167	173	DDIVTVE	7
9	180	186	DGTVFDS	7
10	195	204	TFPLSQVIPG	10
11	219	226	TFYIPSNL	8
12	240	253	NATLVFDVKLVKIG	14

---

**Reference:** [Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276\(1-2\):172-4.](#)

**Scale values:** A:1.064, C:1.412, D:0.866, E:0.851, F:1.091, G:0.874, H:1.105, I:1.152, K:0.93, L:1.25, M:0.826, N:0.776, P:1.064, Q:1.015, R:0.873, S:1.012, T:0.909, V:1.383, W:0.893, Y:1.161